UNITED STATES DISTRICT COURT
WESTERN DISTRICT OF WISCONSIN

PROMEGA CORPORATION,

Plaintiff,

MAX-PLANCK-GESELLSCHAFT ZUR FORDERUNG DER WISSENSCHAFTEN E.V.,

Involuntary Plaintiff,

v.

LIFE TECHNOLOGIES CORPORATION, INVITROGEN IP HOLDINGS, INC., and APPLIED BIOSYSTEMS, INC.,

Defendants.

Case No.: 10-CV-281

EXPERT REPORT OF KATHLEEN M. MURPHY, Ph.D.

The following information is provided pursuant to Rule 26(a)(2)(B):

1. A complete statement of all opinions to be expressed by me at trial and the basis and reasons for all such opinions is attached hereto as **Attachment 1**. I reserve the right to supplement this report, as appropriate, after reviewing any further information provided in the case.

2. The material and information considered by me in forming the opinions noted in paragraph one are identified in Attachment 1.

3. A copy of my curriculum vitae, which includes my qualifications and a list of all publications authored by me within the preceding ten (10) years is attached hereto as Attachment 2.

4. I am currently Director of Clinical Laboratory Operations at ProPath.

5. I have not provided any testimony in the last four years.

6. I am being compensated for this report at a rate of $200/hour.

7. Having been informed that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the U.S. Code, I declare under penalty of perjury that the following is true and correct.

Dated this 8th day of July, 2011.

Kathleen M. Murphy, Ph.D.

ATTACHMENT 1

TO EXPERT REPORT OF KATHLEEN MURPHY

If called to testify in this case, I will express the following opinions at trial, the basis and reasons for which are set forth below and detailed in the documentation identified below. I reserve the right to supplement these opinions in the event of new information.

1. In preparing this report, I reviewed publications, particularly my own publications, utilizing STR multiplex technology in the clinical setting. In some of my own publications, I utilized commercially available kits. These kits are used extensively for applications in the forensic and paternity fields. However, uses of STR technology today in the clinical setting "are well established and include bone marrow engraftment analysis, diagnosis of hydatidiform moles, assessment of maternal cell contamination in prenatal specimens" as well as "use in the resolution of specimen labeling/identification issues . . . and extraneous tissue contaminant issues . . ." See J. Pfeifer et al, "The Changing Spectrum of DNA-based Specimen Provenance Testing in Surgical Pathology," *Am. J. Clin. Path.*, 135:132 (2011) (attached as Exhibit 1) (see introduction section). I have published in a number of these areas.
2. For example, I am a co-author on the publication by Liang et al., in the Journal of Molecular Diagnostics, in which we applied STR multiplexing at Johns Hopkins University to examine bone marrow engraftment using commercially available kits from ABI. See Liang et al., "Application of Traditional Clinical Pathology

Quality Control Techniques to Molecular Pathology, *J. Mol. Diag.* 10:142 at 143 (2008) (attached hereto as Exhibit 2). As noted in the introduction section of this publication: "Allogeneic bone marrow transplantation is performed for the treatment of many hematological malignancies as well as other diseases . . ." Where the donor and recipient are not a perfect tissue match, i.e. the graft is genetically non-identical, the transplant is called an "allogeneic" transplant.

3. In some situations, it is desired that the bone marrow transplant should result in the production of blood cells strictly from the donor graft. To achieve this, the recipient must receive treatment so that their bone marrow is ablated prior to transplantation. Such treatment has a number of problems. First, since it is cytotoxic, the treatment can weaken an already sick patient, putting them at risk for other problems. Second, it is not always successful, i.e. complete ablation is not achieved.

4. Because of these limitations, and other advances in the field, a non-ablative approach has been developed. Using this technique, the recipient is treated with a regimen with reduced cytotoxicity, which decreases, but may not eliminate the recipient's bone marrow. This technique can be successful because donor cells can mount a "graft-vs-host" immune response against proteins on the recipient's tumor cells. While not without risk, this approach offers a potentially curative procedure to patients who would not tolerate high-dose cytotoxic conditioning regimens.

5. Regardless of whether an ablative or non-ablative pre-transplant regimen is used, following bone marrow transplantation, the recipient may produce their own

(host) as well as donor blood cells. As a result, there is what is called "chimerism," i.e. a mixture of two types of cells. Chimerism analysis provides quantitative information about the transplant and can serve as a prognostic factor.

6. Detecting chimerism can be done in a variety of ways. As noted in the introduction section of Liang et al.: "The success of engraftment has long been evaluated using many different techniques . . . More recently, . . . the extent of engraftment [has been determined] by analyzing microsatellites amplified with fluorescent primers and resolved on a commercially available DNA sequencer." This last sentence is referring to STR multiplexing. As indicated in the publication (p. 144), the commercially available machine we used at Johns Hopkins was the ABI PRISM 3100 Genetic Analyzer. The ABI PRISM instrument can quantitate the peak area and/or height for each of the amplified alleles [donor alleles and host (patient) alleles]. This allows for an accurate calculation of the percentage of cells in the specimen that are derived from the donated transplant versus from the host (patient). For example, a patient report may indicate that the submitted specimen was composed of 5% patient, 50% patient, or 95% patient, etc. This allows the clinician to monitor the patient and identify when a change in chimerism has occurred.

7. Measuring chimerism using STR multiplexing can be viewed as a type of tissue typing. It is not for the purpose of human identity because, after all, the identity of the donor and recipient in the transplant is known. Rather, it is to quantitatively assess and monitor the success or failure of transplant.

8. Monitoring bone marrow engraftment using chimerism analysis is important for several reasons including:
    a. Identification of complete failure to engraft donor cells.
    b. Identification of failure to engraft particular sub-sets of donor cells (primarily T-cells).
    c. Detecting and monitoring residual disease
    d. Detecting disease relapse.
9. Chimerism analysis is generally performed serially. The presence of recipient cells following transplantation (particularly a non-ablative transplant) may not indicate residual disease or relapse because normal/non-malignant recipient cells may be produced post-transplant. Therefore, serial analyses are performed to monitor for an <u>increase</u> in recipient cells, which is associated with the reappearance of the underlying disease. See Pulsipher et al., *Biol. Blood Marrow Transplant*, 15:62 (2009) at p. 65 (attached as Exhibit 3).
10. The time interval between a change in chimerism and relapse can be very short. Therefore, serial analysis of chimerism by STR-PCR needs to be done frequently during the first 100 to 200 days after transplantation, when most relapses occur. See Pulsipher et al., *Biol. Blood Marrow Transplant*, 15:62 (2009) at p. 66 (attached as Exhibit 3). Some groups emphasize repeated testing in the first month post-transplant. See Kristt et al., Assessing Quantitative Chimerism Longitudinally, *Bone Marrow Transplant*, 39:255 (2007) at p. 266 (attached as Exhibit 4). Where other markers are not available, sequential analysis of the

percent of chimerism "may offer the only evidence on which sub-clinical relapse of disease can be assessed . . . " Kristt et al., at page 261.

11. At Johns Hopkins, STR multiplexing using the ABI kit we describe in Liang et al. was done on virtually all donors and recipients of transplants. Indeed, it is part of a "routine workup before the patient's bone marrow transplant . . ." See K. Murphy, Constitutional Duplication of a Region of Chromosome Yp encoding AMELY, PRKY, and TBL1Y, *J. Mol. Diag.*, 9:408 (2007) (attached as Exhibit 5) (see Results and Discussion Section). Moreover, the recipients were tested repeatedly post-transplant.

12. There are several different types of white blood cells (B-cells, T-cells, NK-cells, granulocytes, monocytes, etc.). In some cases, chimerism analysis of particular subsets of cells may provide important information. Several groups have found that analysis of T-cells is useful for early detection of relapse and for predicting graft versus host disease. In order to perform this analysis, the recipient's post-transplant blood specimen is processed to separate different subsets of cells. Each subset may be analyzed separately for chimerism. Thus one specimen may be used for multiple chimerism analyses.

13. As noted in Liang et al., there are instances where "decisions to alter treatment are based on major shifts in the degree of chimerism . . .". Liang et al., *J. Mol. Diag.* 10:142 at 145 (2008) (attached hereto as Exhibit 2). In some cases where analysis of chimerism indicates a relapse risk, relapse can be prevented by changing therapy, e.g. withdrawing immune suppression and/or by administering infusions

of donor cells (such as donor lymphocytes). See Pulsipher et al., *Biol. Blood Marrow Transplant*, 15:62 (2009) at p. 65 (attached as Exhibit 3).

14. Thus, in the clinical field of bone marrow transplantation, STR multiplexing to monitor bone marrow engraftment has become an important tool for the physician to increase the chances of transplant success to treat malignancies. While there are other tests that might be used, "the overwhelming majority of laboratories" continue to use STR multiplexing in this manner. Liang et al., *J. Mol. Diag.* 10:142 at 142 (2008) (attached hereto as Exhibit 2) (see introduction).

15. Transplantation is not the only clinical field where STR multiplexing is useful. As noted above, STR multiplexing can be very useful to genotype hydatidiform moles. See K. Murphy et al., Molecular Genotyping of Hydatidiform Moles, *J. Mol. Diag*. 11:598 (2009) (attached hereto as Exhibit 6). Hydatidiform moles are an abnormal product of conception (POC) which implants in the uterus. A complete hydatidiform mole (CHM) is caused by a single sperm combining with an egg which has lost its DNA, but where the sperm has formed a "complete" 46 chromosome set (i.e. diploid, with both sets being paternal in origin). A partial hydatidiform mole (PHM) is not diploid, and is most often triploid (with one maternal set and two paternal sets of chromosomes).

16. Distinction of hydatidiform moles from non-molar specimens and the sub-classification of hydatidiform moles as CHM, PHM, are important for both clinical practice and investigational studies. Accurate classification is critical to ascertaining the woman's risk of persistent gestational trophoblastic disease (GTD) and determining the appropriate nature and duration of clinical follow-up

care. Both under-diagnosis and over-diagnosis of hydatidiform moles can result in faulty estimation of the risk of persistent GTD and improper clinical management.

17. The risk of persistent gestational trophoblastic disease (GTD) and hence, clinical management, differs for CHMs, PHMs, and non-molar specimens. Based on well-defined cases in the modern literature, the risk of persistent GTD is 15-20%, following CHM, 0.2-4% following PHM, and ≤ 0.0002% following non-molar spontaneous abortions. Persistent GTD following a hydatidiform mole can present as an invasive mole, as well as a type of cancer, choriocarcinoma. Approximately 10 – 20% of women will require chemotherapy treatment because of persistent GTD following a CHM.

18. As noted in my paper (see the introduction section), diagnosis of hydatidiform moles (HM) "based solely on morphology suffers from poor interobserver reproducibility" even where the pathologist is experienced. Other groups have also reported "poor interobserver and intraobserver reproducibility." See F. Lipata et al., Precise DNA Genotyping Diagnosis of Hydatidiform Mole, Obstetrics & Gynec. 115: 784 (2010) (introduction section) (attached hereto as Exhibit 7). While a variety of techniques have been tried to improve diagnosis, "analysis of the type provided by STR genotyping offers greater diagnostic discriminatory capability . . ." See K. Murphy et al., Molecular Genotyping of Hydatidiform Moles, *J. Mol. Diag*. 11:598 (2009) (attached hereto as Exhibit 6).

19. As noted on page 599 of my publication, the commercially available "AmpFlSTR Profiler Kit (Applied Biosystems, Foster City, CA) was used for this analysis."

We found the kit to be "applicable to routine practice for classifying molar specimens." See K. Murphy et al., Molecular Genotyping of Hydatidiform Moles, *J. Mol. Diag.* 11:598 at page 604 (2009) (attached hereto as Exhibit 6).

20. A variety of molecular techniques have been used to improve diagnosis of hydatidiform moles, including cytogenetic analysis (karyotyping), determination of ploidy by flow cytometry, and fluorescent in situ hybridization (FISH). In my opinion, STR genotyping offers greater diagnostic discriminatory capability than other genetic techniques in that CHMs, PHMs, and non-molar specimens can be specifically distinguished from one another based on identification of the parental source of polymorphic alleles and their ratios. In particular, this analysis can discern androgenetic diploidy (two paternal chromosomse sets), diandric triploidy (one maternal and two paternal chromosome sets), and biparental diploidy (one maternal and one paternal chromosome set) to rigorously diagnose and distinguish CHMs, PHMs, and non-molar specimens, respectively. See B. Ronnett *et al.*, "Hydatidiform Moles: Ancillary Techniques to Refine Diagnosis," Int. J. Gyn. Path. 30:101 (2011) (Exhibit 8).

21. Classifying molar specimens using STR multiplexing can be viewed as a type of tissue typing. It is not for the purpose of human identity because, after all, the identity of the person with molar pregnancy is known. It is also not for the purpose of determining the father. Rather, it is performed to make the most accurate diagnosis, and to assess the woman's risk for persistent disease that may require chemotherapeutic treatment.

22. Interobserver variation with histology is not unique to hydatidiform moles or trophoblastic tissue. Diagnostic dilemmas exist for other types of tissue and diseases. Ancillary testing can be important to make accurate diagnoses, prognoses, and treatment decisions. As noted in the introduction of a paper I co-authored: "the histologic distinction between oligodendroglioma and astrocytoma is often highly subjective . . . and there has been significant interobserver variation in the diagnosis . . ." K. Hatanpaa et al., Molecular Diagnosis of Oligodendroglioma in Paraffin Sections, *Lab. Invest.* 83:419 (2003) (attached as Exhibit 9). Accurate differentiation of these tumor types is important since their prognosis and response to therapeutic intervention differ significantly. One ancillary technique used to distinguish and accurately diagnose these tumors is to analyze the tumor for loss of genetic material. Specifically, oligodendroglioma tumors, but not astrocytomas, are characterized by loss chromosome arms 1p and 19q. In our paper we extracted DNA from tumors that had been paraffin embedded and performed STR multiplexing using dinucleotide STR markers located on chromosome arms 1p and 19q. We demonstrated that analysis of these STR markers correlated well with other methods for the detection of loss of chromosome arms 1p and 19q. This method is currently used in the Johns Hopkins Molecular Diagnostics Laboratory for the purpose of accurately differentiating oligodendroglioma tumor from other brain tumors.

23. Differentiating oligodendroglioma tumors from other brain tumors is not human identity testing since the source of the tissue is known, i.e. there is no need for a comparison in order to match the sample with the patient. The STR multiplexing

results from the DNA of a single known person (the patient) are used to determine whether the tumor is an oligodendroglioma.

24. Processing of tissues for pathologic review is a fairly manual process, with risk of incorrect specimen identification, and specimen contamination. During processing, tissue fragments from one case can be associated with the tissue block of another specimen. This can occur "in the cutting room when a tissue fragment from one case remains on a surface . . . and is inadvertently transferred into another specimen's cassette." K. Berg and K. Murphy, "Floaters in Surgical Pathology Tissues, *Path. Case Rev*. 8:103 (2003) (attached hereto as Exhibit 10) (see introduction section). Our work showed that STR multiplexing with commercially available ABI kits can assist in sorting out the contamination. This testing can be an important quality control measure to avoid incorrect results due to tissue cross-contamination.

25. Using STR multiplexing to identify and resolve contamination, or rule it out, is not limited to the clinical pathology laboratory. STR multiplexing can assist in confirming that cell lines are genetically unique; this is useful in a variety of settings, including clinical research and basic research. In one study, STR multiplexing with commercially available ABI kits was performed on 40 reported thyroid cancer-derived cell lines, only to reveal that a) many were not unique, and b) some were not even of thyroid origin. See R. Schweppe et al., Deoxyribonucleic Acid Profiling Analysis of 40 Human Thyroid Cancer Cell Lines Reveals Cross-Contamination Resulting in Cell Line Redundancy and Misidentification, *J. Clin. Endocrinol. Metab*. 93:4331 (2008) (attached hereto as

Exhibit 11) (see Abstract). As noted in this report (p. 4332), the NIH now recognizes this problem and requires cell authentication with grant applications. Indeed, commercial companies that supply cell lines provide corresponding STR data so that researchers can ensure the proper identity of a cell line even after long term passage in cell culture.

26. Cell line authentication is yet another type of tissue typing. It is not human identity testing because the human source of the cell line is not sought. Rather, it is a measure of the genetic integrity and genetic uniqueness of the cell line.

27. The information provided here demonstrates that STR testing can be used for a variety of different purposes. The applications for STR testing have expanded as we have gained an increased understanding of genetics and of disease states. The ease of use of commercially available multiplex STR kits, and the wealth of information they can provide, have made them an appealing platform for testing. The intent of these clinical and research studies is not to identify the individual from whom a specimen originated, but to identify specific information about the genetic composition of the specimen, which can be used to make a diagnosis, monitor a bone marrow transplant patient, or resolve a tissue contamination dilemma, etc.

Kathleen M Murphy, PhD
1355 River Bend Drive, Dallas, TX, 75247
Office phone: 214-237-1681, email: kathy.murphy@propath.com

PROFESSIONAL EXPERIENCE

2010- present	Director, Clinical Laboratory Operations ProPath Services, Dallas, TX
2008 - 2009	Associate Professor Departments of Pathology and Oncology The Johns Hopkins School of Medicine, Baltimore, MD
2005 - 2008	Assistant Professor, Department of Oncology The Johns Hopkins School of Medicine, Baltimore, MD
2002 - 2008	Assistant Professor, Department of Pathology The Johns Hopkins School of Medicine, Baltimore, MD
2001 - 2002	Instructor, Department of Pathology The Johns Hopkins School of Medicine, Baltimore, MD
2001 - 2008	Lecturer, Graduate Program in Biotechnology The Johns Hopkins Univ. School of Arts and Sciences, Baltimore, MD
1988 – 1993	Medical Technologist, Immunology Laboratory University of Virginia, Charlottesville, VA

EDUCATION AND TRAINING

1988	B.S., Medical Technology George Mason University, Fairfax, VA
1988	Medical Technology Certificate University of Virginia Medical Center, Charlottesville, VA
1999	Ph.D. Thesis: “Function of Bcl-2 and Bax in the regulation of apoptosis”, Richard B. Lock, Ph.D., mentor Department of Microbiology and Immunology University of Louisville, Louisville, KY
2000 - 01	Postdoctoral Fellowship, Molecular Pathology The Johns Hopkins University School of Medicine, Baltimore, MD

AWARDS, HONORS

1988	Golden Key National Honor Society
1988	Joy Austin Medical Technology Scholarship
1998	University of Louisville Education Abroad Scholarship
1999	Women in Cancer Research-AACR Leventhal Scholar Award
1999	American Association for Cancer Research (AACR) Young Investigator Award
2000	Graduate Dean’s Citation, University of Louisville
2001	Association of Molecular Pathology (AMP) Young Investigator Award

CERTIFICATION

1988	M.T. (ASCP) 177205
1994	Specialist in Immunology (ASCP) 291

PROFESSIONAL SOCIETIES

1988 - present	American Society of Clinical Pathology member
1998 - present	American Association for Cancer Research member
1999 - present	Association for Molecular Pathology member
2003 - 2005	American Society for Investigative Pathology member
2006 – 2010	Association for Molecular Pathology Web Library Editor

---

CLINICAL ACTIVITIES

Director, Clinical Laboratory Operations, ProPath 1/10 - present

- Establish and implement laboratory goals for test development and process improvement
- Assay validation
- Oversight of quality control and quality assurance
- General laboratory administration, budget oversight, clinical licensure
- Responsibility for medical technologists' career development and advancement

Director, JHU Molecular Diagnostics Laboratory 11/03 – 12/09

- Attend on the Molecular Diagnostics service (review all data, sign lab reports)
- Establish and implement laboratory goals for test development and process improvement
- Assay validation (primarily "homebrew")
- Oversight of quality control and quality assurance
- General laboratory administration, budget oversight, clinical licensure
- Responsibility for medical technologists' career development and advancement

---

RESEARCH ACTIVITIES

Peer-reviewed Publications

1. Elliott MJ, **Murphy KM**, Stribinskiene L, Ranganathan V, Sturges E, Farnsworth ML, Lock RB: Bcl-2 inhibits early apoptotic events and reveals post-mitotic multinucleation without affecting cell cycle arrest in human epithelial tumor cells exposed to etoposide. Cancer Chemother Pharmacol 1999, 44:1-11
2. **Murphy KM**, Streips UN, Lock RB: Bax membrane insertion during Fas(CD95)-induced apoptosis precedes cytochrome c release and is inhibited by Bcl-2. Oncogene 1999, 18:5991-9
3. **Murphy KM**, Streips UN, Lock RB: Bcl-2 inhibits a Fas-induced conformational change in the Bax N terminus and Bax mitochondrial translocation. J Biol Chem 2000, 275:17225-8

4. **Murphy KM**, Ranganathan V, Farnsworth ML, Kavallaris M, Lock RB: Bcl-2 inhibits Bax translocation from cytosol to mitochondria during drug-induced apoptosis of human tumor cells. Cell Death Differ 2000, 7:102-11
5. Berg KD, Brinster NK, Huhn KM, Goggins MG, Jones RJ, Makary A, **Murphy KM**, Griffin CA, Rosenblum-Vos LS, Borowitz MJ, Nousari HC, Eshleman JR: Transmission of a T-cell lymphoma by allogeneic bone marrow transplantation. N Engl J Med 2001, 345:1458-63
6. Peaston AE, Gardaneh M, Franco AV, Hocker JE, **Murphy KM**, Farnsworth ML, Catchpoole DR, Haber M, Norris MD, Lock RB, Marshall GM: MRP1 gene expression level regulates the death and differentiation response of neuroblastoma cells. Br J Cancer 2001, 85:1564-71
7. Su GH, Bansal R, **Murphy KM**, Montgomery E, Yeo CJ, Hruban RH, Kern SE: ACVR1B (ALK4, activin receptor type 1B) gene mutations in pancreatic carcinoma. Proc Natl Acad Sci U S A 2001, 98:3254-7
8. **Murphy KM**, Brune KA, Griffin C, Sollenberger JE, Petersen GM, Bansal R, Hruban RH, Kern SE: Evaluation of candidate genes MAP2K4, MADH4, ACVR1B, and BRCA2 in familial pancreatic cancer: deleterious BRCA2 mutations in 17%. Cancer Res 2002, 62:3789-93
9. **Murphy KM**, Eshleman JR: Simultaneous sequencing of multiple polymerase chain reaction products and combined polymerase chain reaction with cycle sequencing in single reactions. Am J Pathol 2002, 161:27-33
10. Sohn TA, Bansal R, Su GH, **Murphy KM**, Kern SE: High-throughput measurement of the Tp53 response to anticancer drugs and random compounds using a stably integrated Tp53-responsive luciferase reporter. Carcinogenesis 2002, 23:949-57
11. Hatanpaa KJ, Burger PC, Eshleman JR, **Murphy KM**, Berg KD: Molecular diagnosis of oligodendroglioma in paraffin sections. Lab Invest 2003, 83:419-28
12. Hempen PM, Zhang L, Bansal RK, Iacobuzio-Donahue CA, **Murphy KM**, Maitra A, Vogelstein B, Whitehead RH, Markowitz SD, Willson JK, Yeo CJ, Hruban RH, Kern SE: Evidence of selection for clones having genetic inactivation of the activin A type II receptor (ACVR2) gene in gastrointestinal cancers. Cancer Res 2003, 63:994-9
13. **Murphy KM**, Geiger T, Hafez MJ, Eshleman JR, Griffin CA, Berg KD: A single nucleotide primer extension assay to detect the APC I1307K gene variant. J Mol Diagn 2003, 5:222-6
14. **Murphy K**, Hafez M, Philips J, Yarnell K, Gutshall K, Berg K: Evaluation of temperature gradient capillary electrophoresis for detection of the Factor V Leiden mutation: coincident identification of a novel polymorphism in Factor V. Mol Diagn 2003, 7:35-40
15. **Murphy KM**, Levis M, Hafez MJ, Geiger T, Cooper LC, Smith BD, Small D, Berg KD: Detection of FLT3 internal tandem duplication and D835 mutations by a multiplex polymerase chain reaction and capillary electrophoresis assay. J Mol Diagn 2003, 5:96-102
16. Ansari-Lari MA, Yang CF, Tinawi-Aljundi R, Cooper L, Long P, Allan RH, Borowitz MJ, Berg KD, **Murphy KM**: FLT3 mutations in myeloid sarcoma. Br J Haematol 2004, 126:785-91

17. Blakemore K, Hattenburg C, Stetten G, Berg K, South S, **Murphy K**, Jones R: In utero hematopoietic stem cell transplantation with haploidentical donor adult bone marrow in a canine model. Am J Obstet Gynecol 2004, 190:960-73
18. Cao D, Hustinx SR, Sui G, Bala P, Sato N, Martin S, Maitra A, **Murphy KM**, Cameron JL, Yeo CJ, Kern SE, Goggins M, Pandey A, Hruban RH: Identification of novel highly expressed genes in pancreatic ductal adenocarcinomas through a bioinformatics analysis of expressed sequence tags. Cancer Biol Ther 2004, 3:1081-9; discussion 1090-1
19. Kochevar GJ, Brody JR, Kadkol SS, **Murphy KM**, Pasternack GR: Identification of a functional mutation in pp32r1 (ANP32C). Hum Mutat 2004, 23:546-51
20. Rogers CD, Couch FJ, Brune K, Martin ST, Philips J, **Murphy KM**, Petersen G, Yeo CJ, Hruban RH, Goggins M: Genetics of the FANCA gene in familial pancreatic cancer. J Med Genet 2004, 41:e126
21. Smith BD, Levis M, Beran M, Giles F, Kantarjian H, Berg K, **Murphy KM**, Dauses T, Allebach J, Small D: Single-agent CEP-701, a novel FLT3 inhibitor, shows biologic and clinical activity in patients with relapsed or refractory acute myeloid leukemia. Blood 2004, 103:3669-76
22. Wang M, **Murphy KM**, Kulesza P, Hatanpaa KJ, Olivi A, Tufaro A, Erozan Y, Westra WH, Burger PC, Berg KD: Molecular diagnosis of metastasizing oligodendroglioma: a case report. J Mol Diagn 2004, 6:52-7
23. Batista DA, Hawkins A, **Murphy KM**, Griffin CA: BCR/ABL rearrangement in two cases of Philadelphia chromosome negative chronic myeloid leukemia: deletion on the derivative chromosome 9 may or not be present. Cancer Genet Cytogenet 2005, 163:164-7
24. Cao D, Hafez M, Berg K, **Murphy K**, Epstein JI: Little or no residual prostate cancer at radical prostatectomy: vanishing cancer or switched specimen?: a microsatellite analysis of specimen identity. Am J Surg Pathol 2005, 29:467-73
25. Jain SK, Persaud D, Perl TM, Pass MA, **Murphy KM**, Pisciotta JM, Scholl PF, Casella JF, Sullivan DJ: Nosocomial malaria and saline flush. Emerg Infect Dis 2005, 11:1097-9
26. Levis M, **Murphy KM**, Pham R, Kim KT, Stine A, Li L, McNiece I, Smith BD, Small D: Internal tandem duplications of the FLT3 gene are present in leukemia stem cells. Blood 2005, 106:673-80
27. Mamelak AJ, Kowalski J, **Murphy K**, Yadava N, Zahurak M, Kouba DJ, Howell BG, Tzu J, Cummins DL, Liegeois NJ, Berg K, Sauder DN: Downregulation of NDUFA1 and other oxidative phosphorylation-related genes is a consistent feature of basal cell carcinoma. Exp Dermatol 2005, 14:336-48
28. **Murphy KM**, Berg KD, Geiger T, Hafez M, Flickinger KA, Cooper L, Pearson P, Eshleman JR: Capillary electrophoresis artifact due to eosin: implications for the interpretation of molecular diagnostic assays. J Mol Diagn 2005, 7:143-8
29. **Murphy KM**, Berg KD, Eshleman JR: Sequencing of genomic DNA by combined amplification and cycle sequencing reaction. Clin Chem 2005, 51:35-9
30. Rand V, Huang J, Stockwell T, Ferriera S, Buzko O, Levy S, Busam D, Li K, Edwards JB, Eberhart C, **Murphy KM**, Tsiamouri A, Beeson K, Simpson AJ, Venter JC, Riggins GJ, Strausberg RL: Sequence survey of receptor tyrosine kinases reveals mutations in glioblastomas. Proc Natl Acad Sci U S A 2005, 102:14344-9
31. Swierczynski SL, Hafez MJ, Philips J, Higman MA, Berg KD, **Murphy KM**: Bone marrow engraftment analysis after granulocyte transfusion. J Mol Diagn 2005, 7:422-6

32. Batista DA, Vonderheid EC, Hawkins A, Morsberger L, Long P, **Murphy KM**, Griffin CA: Multicolor fluorescence in situ hybridization (SKY) in mycosis fungoides and Sezary syndrome: search for recurrent chromosome abnormalities. Genes Chromosomes Cancer 2006, 45:383-91
33. Bian Y, Matsubayashi H, Pin-Li C, Abe T, Canto M, **Murphy KM**, Goggins M: Detecting Low-Abundance p16 and p53 Mutations in Pancreatic Juice Using A Novel Assay: Heteroduplex Analysis of Limiting Dilution PCRs. Cancer Biol Ther 2006, 5:1392-9
34. Brody JR, Hucl T, Gallmeier E, Winter JM, Kern SE, **Murphy KM**: Genomic Copy Number Changes Affecting the Thymidylate Synthase (TYMS) Gene in Cancer: A Model for Patient Classification to Aid Fluoropyrimidine Therapy. Cancer Res 2006, 66:9369-73
35. Griffin CA, Burger P, Morsberger L, Yonescu R, Swierczynski S, Weingart JD, **Murphy KM**: Identification of der(1;19)(q10;p10) in five oligodendrogliomas suggests mechanism of concurrent 1p and 19q loss. J Neuropathol Exp Neurol 2006, 65:988-94
36. Montgomery E, Mamelak AJ, Gibson M, Maitra A, Sheikh S, Amr SS, Yang S, Brock M, Forastiere A, Zhang S, **Murphy KM**, Berg KD: Overexpression of claudin proteins in esophageal adenocarcinoma and its precursor lesions. Appl Immunohistochem Mol Morphol 2006, 14:24-30
37. **Murphy KM**, Zhang S, Geiger T, Hafez MJ, Bacher J, Berg KD, Eshleman JR: Comparison of the microsatellite instability analysis system and the Bethesda panel for the determination of microsatellite instability in colorectal cancers. J Mol Diagn 2006, 8:305-11
38. Nayer H, **Murphy KM**, Hawkins AL, Long PP, Gillison M, Borowitz M, Griffin CA: Clonal cytogenetic abnormalities and BCL2 rearrangementin interdigitating dendritic cell sarcoma. Leuk Lymphoma 2006, 47:2651-4
39. Duelli DM, Padilla-Nash HM, Berman D, **Murphy KM**, Ried T, Lazebnik Y: A Virus Causes Cancer by Inducing Massive Chromosomal Instability through Cell Fusion. Curr Biol 2007, 17:431-7
40. Jobbagy Z, van Atta R, **Murphy KM**, Eshleman JR, Gocke CD: Evaluation of the Cepheid GeneXpert BCR-ABL Assay. J Mol Diagn 2007, 9:220-7
41. Petersen SM, Gendelman M, **Murphy KM**, Torbenson M, Jones RJ, Althaus JE, Stetten G, Bird C, Blakemore KJ: Use of T-Cell Antibodies for Donor Dosaging in a Canine Model of in utero Hematopoietic Stem Cell Transplantation. Fetal Diagn Ther 2007, 22:175-179

42. **Murphy KM**, Cohen JS, Goodrich A, Long PP, and Griffin CA. Constitutional Duplication of a Region of Chromosome Yp Encoding *AMELY*, *PRKY*, and *TBL1Y*; Implications for Sex Chromosome Analysis and Bone Marrow Engraftment Analysis. J Mol Diagn; J Mol Diagn. 2007,9 3:408-13
43. Patel AS*, **Murphy KM***, Hawkins AL, Cohen JS, Long PP, Perlman EJ, Griffin CA. RANBP2 and CLTC Involved in ALK Rearrangements in Inflammatory Myofibroblastic Tumors. (*co-first authors). Cancer Genet Cytogenet. 2007, 176 2:107-14
44. Lin M, Rich RG, Shipley RF, Hafez MJ, **Murphy KM**, Gocke CD, and Eshleman JR. A molecular fraction collecting tool for the ABI 310 automated sequencer. J Mol Diagn. 2007, 9 5:598-603

45. Karanjawala ZE, Illei P, Ashfaq R, Infante J, **Murphy K**, Pandey A, Schulick R, Winter J, Sharma R, Maitra A, Goggins M, Hruban R: New Markers of Pancreatic Cancer Identified Through Differential Gene Expression Analyses: Claudin 18 and Annexin A8. Am J Surg Pathol. 2008, 32 2:188-96
46. Liang SL, Lin MT, Hafez MJ, Gocke CD, **Murphy KM**, Sokoll LJ, Eshleman JR. Application of Traditional Clinical Pathology Quality Control Techniques to Molecular Pathology. J Mol Diagn. 2008, 10 2:142-6
47. **Murphy KM**, Chen F, Clark DP. Identification of immunohistochemical biomarkers for papillary thyroid carcinoma using gene expression profiling. Hum Pathol. 2008, 39 3:420-6
48. Cho, E., Schiffer, J., Murphy, K, Smith, BD. Isolated granulocytic sarcoma: case reports of three rare presentations and review. Clinical Leukemia. 2008; Vol. 2, No. 4, 275-279.
49. McConnell TG, **Murphy KM**, Hafez M, Vang, R, Ronnett BM. Diagnosis and Subclassification of Hydatidiform Moles Utilizing p57 Immunohistochemistry and Molecular Genotyping: Validation and Prospective Analysis in Routine and Consultation Practice Settings with Development of an Algorithmic Approach. Am J Surg Pathol. 2009 Jun;33(6):805-817.
50. Smith BD, Kasamon YL, Kowalski J, Gocke C, **Murphy K**, Miller CB, Garrett-Mayer E, Tsai HL, Qin L, Chia C, Biedrzycki B, Harding TC, Tu GH, Jones R, Hege K, Levitsky HI. K562/GM-CSF immunotherapy reduces tumor burden in chronic myeloid leukemia patients with residual disease on imatinib mesylate. Clin Cancer Res. 2010 Jan 1;16(1):338-47.
51. Jinawath N, Norris-Kirby A, Smith BD, Gocke CD, Batista DA, Griffin CA, and **Murphy KM**. A rare e14a3 (b3a3) BCR-ABL fusion transcript in chronic myeloid leukemia: diagnostic challenges in clinical laboratory practice.J Mol Diagn. 2009 Jul;11(4):359-63. Epub 2009 Jun 4.
52. McConnell TG, Norris-Kirby A, Hagenkord JM, Ronnett BM, and **Murphy KM**. Complete Hydatidiform Mole With Retained Maternal Chromosomes 6 and 11. Am J Surg Pathol. 2009 Sep;33(9):1409-15.
53. **Murphy KM**, Griffin CA, Ferguson W, and Vnencak-Jones CL. Constitutional Amplification of Regions of Yp and Yq in a Patient with Aplastic Anemia and Hypogonadism. Submitted
54. **Murphy KM**, McConnell TG, Hafez MJ, Vang R, Ronnett BM. Molecular Genotyping of Hydatidiform Moles: Analytic Validation of a Multiplex Short Tandem Repeat (STR) Assay. J Mol Diagn. 2009 Nov;11(6):598-605.
55. Pratz KW, Sato T, **Murphy KM**, Stine A, Rajkhowa T, Levis M. FLT3-mutant allelic burden and clinical status are predictive of response to FLT3 inhibitors in AML. Blood. 2010 Feb 18;115(7):1425-32. Epub 2009 Dec 10.
56. Weekes CD, Nallapareddy S, Rudek MA, Norris-Kirby A, Laheru D, Jimeno A, Donehower RC, **Murphy KM**, Hidalgo M, Baker SD, Messersmith WA. Thymidylate synthase (TYMS) enhancer region genotype-directed phase II trial of oral capecitabine for 2nd line treatment of advanced pancreatic cancer. Invest New Drugs. 2010 Mar 23. [Epub ahead of print]
57. Norris-Kirby A, Hagenkord JM, Kshirsagar MP, Ronnett BM, and **Murphy KM**. Abnormal villous morphology associated with triple trisomy of paternal origin. J Mol Diagn. 2010 Jul;12(4):525-9. Epub 2010 Apr 22.

58. Tsiatis AC, Kirby AN, Rich RG, Hafez MJ, Gocke CD, Eshleman JR, and **Murphy KM**. Comparison of Sanger Sequencing, Pyrosequencing, and Melting Curve analysis for the detection of *KRAS* Mutations: Diagnostic and Clinical Implications J Mol Diagn. 2010 Jul;12(4):425-32. Epub 2010 Apr 29.

59. Yap KL, Hafez MJ, Mao TL, Kurman RJ, **Murphy KM**, Shih IeM. Lack of a y-chromosomal complement in the majority of gestational trophoblastic neoplasms.J Oncol. 2010;2010:364508. Epub 2010 Feb 21.

60. Li F, Shen Y, Köhler U, Sharkey FH, Menon D, Coulleaux L, Malan V, Rio M, McMullan DJ, Cox H, Fagan KA, Gaunt L, Metcalfe K, Heinrich U, Hislop G, Maye U, Sutcliffe M, Wu BL, Thiel BD, Mulchandani S, Conlin LK, Spinner NB, **Murphy KM**, Batista DA. Interstitial microduplication of Xp22.31: Causative of intellectual disability or benign copy number variant? Eur J Med Genet. 2010 Feb 2. [Epub ahead of print]

61. Jinawath N, Morsberger L, Norris-Kirby A, Williams LM, Yonescu R, Argani P, Griffin CA, and **Murphy KM**. Complex rearrangement of chromosomes 1, 7, 21, 22 in Ewing sarcoma. Cancer Genet Cytogenet. 2010 Aug;201(1):42-7.

62. Lin MT, Tseng LH, Rich RG, Hafez MJ, Harada S, **Murphy KM**, Eshleman JR, Gocke CD. Δ-PCR, A Simple Method to Detect Translocations and Insertion/Deletion Mutations. J Mol Diagn. 2011 Jan;13(1):85-92. Epub 2010 Dec 23.

63. Yoon HH, Catalano P, Gibson MK, Skaar TC, Philips S, Montgomery EA, Hafez MJ, Powell M, Liu G, Forastiere AA, Benson AB, Kleinberg LR, **Murphy KM**. Genetic variation in radiation and platinum pathways predicts severe acute radiation toxicity in patients with esophageal adenocarcinoma treated with cisplatin-based preoperative radiochemotherapy: results from the Eastern Cooperative Oncology Group. Cancer Chemother Pharmacol. 2011 Feb 1. [Epub ahead of print]

64. Youens KE, Hosler GA, Washington PJ, Jenevein EP and **Murphy KM**. Clinical Experience with the Cervista HPV HR Assay Correlation of Cytology and HPV Status from 56,501 Specimens. J Mol Diagn. 2011 Mar;13(2):160-6.

65. Yoon HH, Catalano PJ, **Murphy KM**, Skaar TC, Phillips S, Powell M, Montgomery EA, Hafez MJ, Offer SM, Liu G, Meltzer SJ, Wu X, Forastiere AA, Benson AB, Kleinberg LR, Gibson MK. Genetic variation in DNA-repair pathways and response to radiochemotherapy in esophageal adenocarcinoma: a retrospective cohort study of the Eastern Cooperative Oncology Group.BMC Cancer. 2011 May 17;11(1):176. [Epub ahead of print]

66. **Murphy KM**, Discipio C, Wagenfuehr J, Tandy S, Mabray J, Beierl K, Micetich K, Libby AL, and Ronnett BM. Tetraploid Partial Hydatidiform Mole. A Case Report and Review of the Literature. In Press.

Editorial Activities

2001 - present Ad Hoc Reviewer for:

Clinical Cancer Research, Journal of Molecular Diagnostics, Cancer Biology and Therapy, Experimental and Molecular Pathology, Genes, Chromosomes and Cancer, Clinical Chemistry, Genetic Testing, BioTechniques, Gene Therapy and Molecular Biology, Nutrition and Cancer, Analytical and Quantitative Cytology and Histology

Inventions, Patents, Copyrights

2002 Methods and Systems of Nucleic Acid Sequencing
Docket No. 56535-P2 (71699)

EDUCATIONAL ACTIVITIES

Invited Reviews

1. Berg KD and **Murphy KM**: "Floaters" in Surgical Pathology Tissues: Genetic Identity Testing Potential and Pitfalls. Pathol Case Rev 2003, 8:3103-10
2. **Murphy KM** and Berg KD: Mutation and single nucleotide polymorphism detection using temperature gradient capillary electrophoresis.Expert Rev Mol Diagn 2003,3:811-8
3. **Murphy KM** and Ronnett BM. Molecular Analysis of Hydatidiform Moles: Utilizing p57 Immunohistochemistry and Molecular Genotyping to Refine Morphologic Diagnosis. Pathol Case Rev In Press
4. Ronnett BM, Descipio C, **Murphy KM**. Hydatidiform moles: ancillary techniques to refine diagnosis.. Int J Gynecol Pathol. 2011 Mar;30(2):101-16.

Book Chapters

1. Lock RB and **Murphy KM**: Immunodetecting members of the Bcl-2 family of proteins. Methods Mol Med 2005, 111:83-96. (Ed: RD Blumenthal), Humana Press, Inc.
2. **Murphy, KM**. Chimerism Analysis Following Hematopoietic Stem Cell Transplantation. Methods in Molecular Biology: Hematological Malignancies. (Ed: Czader, M), Humana Press Inc. In Press.

Classroom Instruction

1995 - 1997	Medical Microbiology and Immunology, Teaching Assistant University of Louisville School of Medicine, Louisville, KY.
2001 - 2007	Cancer Biology 410.638.01. Course Director Graduate Program in Biotechnology, JHU, Baltimore, MD
2007- 2009	MT-338-01 Molecular and Immunologic Diagnostics. Course Director Stevenson University, Baltimore MD.

Clinical Instruction

Graduate Students: Pathobiology clinical rotation
Pathology Residents: Clinical instruction and didactics
Molecular Pathology Fellows Clinical instruction, didactics, and supervision of clinical projects

Mentoring

High School Students:

Alyssa Vital, Johns Hopkins University Center Scholar Intern Program Summer 2009

Graduate Students:

Christina Cooney, Masters in Biotechnology, 2005

Postdoctoral Fellows:

Adam J Mamelak, M.D., Dermatology Research Fellow, 2002

Jonathan Brody, Ph.D., Post-doctoral Fellow, Department of Oncology 2004-2006

Harry H. Yoon, M.D., Oncology Fellow 2006 – June 2008

INVITED TALKS

02/01	"Identity Testing" Pathology Grand Rounds Resident/Fellows Speakers, JHU, Baltimore, MD
11/01	"Molecular Techniques in the Clinical Laboratory" Kentucky Wesleyan College, Owensboro, KY
05/02	"Familial Pancreatic Cancer: A Role for BRCA2?" GI SPORE Meeting, JHU, Baltimore, MD
05/02	"Novel Sequencing Strategies" GI SPORE Meeting, JHU, Baltimore, MD
09/04	"Molecular Diagnostics of Solid Tumors" G2 Conference, Washington D.C.
05/05	"Molecular Diagnostics: Trials & Tribulations" Pathology Grand Rounds, The Johns Hopkins Hospital, Baltimore, MD
06/05	"Molecular Analysis of Tumor Markers" Clinical Oncology Study Section, Bethesda, MD
11/05	"Theranostic Testing: Prediction of Therapeutic response in Solid Tumors" Assoc. of Molecular Pathology Annual Meeting, Scottsdale, AZ
05/06	"Detection of FLT3 Mutations in the Clinical Lab" FLT3 AML Study Investigators Meeting, Chicago, IL
05/07	"Molecular Diagnostics of Solid Tumors. Lost in Translation?" Research Seminar, Thomas Jefferson University, Philadelphia, PA
09/07	"Molecular Analysis of Hydatidiform Moles" Gynecologic Pathology Seminar, Johns Hopkins, Baltimore, MD
10/07	"FLT3 Mutation Detection" FLT3 AML Study Investigators Meeting, Prague, CZ
11/07	"1p19q LOH testing for Oligodendrogliamas" Assoc. of Molecular Pathology Annual Meeting, Los Angeles, CA
11/07	"Amplification on Chromosome Arm Yp Detected by HD Oligo Array CGH" Agilent Corp Workshop, Assoc. Molec Path Annual Meeting, Los Angeles, CA
2/08	"Molecular Diagnostics that Predict Response to Novel Therapeutics" Biology Seminar Series, Millersville University, Millersville, PA
5/08	"Basics of nucleic acid biochemistry" AMP-AACC Molecular Pathology Essentials. Baltimore, MD
6/08	Molecular Diagnostics

	Beckman Coulter meeting. Philadelphia, PA
10/08	Isolation of Nucleic Acids from Formalin-Fixed Paraffin-Embedded Tissue Beckman coulter Corportate Workshop, Molec Path Annual Meeting, Dallas, TX
11/08	Introduction to Molecular Diagnostics Immucor workshop, Atlanta, GA
03/09	Pharmacogenetic Testing in the Clinical Lab Seminar Series, Stevenson University, Baltimore, MD
05/09	Hydatidiform Moles: Lessons from the Clinical Lab Baltimore Genetics Group Meeting, GBMC, Baltimore MD.
03/10	Molecular Diagnostics of Hydatidiform Moles USCAP Annual Meeting, Washington D.C.
5/10	CVS
08/10	"Molecular Diagnostics for Community Hospital Labs: Hitting Clinical and Financial Home Runs in Infectious Disease and Oncology Testing" Dark Report webinar
11/10	AMP
5/11	Eurogin